

SEP 24 2002

TECH CENTER 1600/2900

## Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER:

09/319,724

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length      The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII      The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length      Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9      Use of n's or Xaa's  
    (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10      Invalid <213>  
    Response      Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11      Use of <220>  
              Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n      n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



1600

## RAW SEQUENCE LISTING

DATE: 09/12/2002

PATENT APPLICATION: US/09/319,724

TIME: 15:45:21

Input Set : A:\aoyama5001.ST25.txt

Output Set: N:\CRF4\09122002\I319724.raw

**Does Not Comply  
Corrected Diskette Needed**

*pp 3-4*

3 <110> APPLICANT: VETIGEN  
 4 LENZEN, Gerlinde  
 5 STROSBURG, Arthur Donny  
 6 SUGASAWA, Toshinari  
 7 MOROOKA, Shigeaki  
 9 <120> TITLE OF INVENTION: MAMMALIAN ICYP (IODOCYANOPINDOLOL) RECEPTOR AND ITS APPLICATIONS

11 <130> FILE REFERENCE: 053356-5001-US  
 13 <140> CURRENT APPLICATION NUMBER: US 09/319,724  
 14 <141> CURRENT FILING DATE: 1999-09-08  
 16 <150> PRIOR APPLICATION NUMBER: EP 96402719.7  
 17 <151> PRIOR FILING DATE: 1996-12-12  
 19 <160> NUMBER OF SEQ ID NOS: 14  
 21 <170> SOFTWARE: PatentIn version 3.1  
 23 <210> SEQ ID NO: 1  
 24 <211> LENGTH: 439  
 25 <212> TYPE: PRT  
 26 <213> ORGANISM: Homo sapiens  
 28 <400> SEQUENCE: 1

30 Met Tyr Ile Asp Asp Leu Pro Ile Trp Gly Ile Val Gly Glu Ala Asp  
 31 1 5 10 15  
 34 Glu Asn Gly Glu Asp Tyr Tyr Leu Trp Thr Tyr Lys Lys Leu Glu Ile  
 35 20 25 30  
 38 Gly Phe Asn Gly Asn Arg Ile Val Asp Val Asn Leu Thr Ser Glu Gly  
 39 35 40 45  
 42 Lys Val Lys Lys Leu Val Pro Asn Thr Lys Ile Gln Met Ser Tyr Ser Val  
 43 50 55 60  
 46 Lys Trp Lys Lys Ser Asp Val Lys Phe Glu Asp Arg Phe Asp Lys Tyr  
 47 65 70 75 80  
 50 Leu Asp Pro Ser Phe Phe Gln His Arg Ile His Trp Phe Ser Ile Phe  
 51 85 90 95  
 54 Asn Ser Phe Met Met Val Ile Phe Leu Val Gly Leu Val Ser Met Ile  
 55 100 105 110  
 58 Leu Met Arg Thr Leu Arg Lys Asp Tyr Ala Arg Tyr Ser Lys Glu Glu  
 59 115 120 125  
 62 Glu Met Asp Asp Met Asp Arg Asp Leu Gly Asp Glu Tyr Gly Trp Lys  
 63 130 135 140  
 66 Gln Val His Gly Asp Val Phe Arg Pro Ser Ser His Pro Leu Ile Phe  
 67 145 150 155 160  
 70 Ser Ser Leu Ile Gly Ser Gly Cys Gln Ile Phe Ala Val Ser Leu Ile  
 71 165 170 175  
 74 Val Ile Ile Val Ala Met Ile Glu Asp Leu Tyr Thr Glu Arg Gly Ser  
 75 180 185 190  
 78 Met Leu Ser Thr Ala Ile Phe Val Tyr Ala Ala Thr Ser Pro Val Asn

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Input Set : A:\aoyama5001.ST25.txt

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79          195          200          205
82 Gly Tyr Phe Gly Gly Ser Leu Tyr Ala Arg Gln Gly Gly Arg Arg Trp
83      210          215          220
86 Ile Lys Gln Met Phe Ile Gly Ala Phe Leu Ile Pro Ala Met Val Cys
87 225          230          235          240
90 Gly Thr Ala Phe Phe Ile Asn Phe Ile Ala Ile Tyr Tyr His Ala Ser
91          245          250          255
94 Arg Ala Ile Pro Phe Gly Thr Met Val Ala Val Cys Cys Ile Cys Phe
95          260          265          270
98 Phe Val Ile Leu Pro Leu Asn Leu Val Gly Thr Ile Leu Gly Arg Asn
99          275          280          285
102 Leu Ser Gly Gln Pro Asn Phe Pro Cys Arg Val Asn Ala Val Pro Arg
103      290          295          300
106 Pro Ile Pro Glu Lys Lys Trp Phe Met Glu Pro Ala Val Ile Val Cys
107 305          310          315          320
110 Leu Gly Gly Ile Leu Pro Phe Gly Ser Ile Phe Ile Glu Met Tyr Phe
111          325          330          335
114 Ile Phe Thr Ser Phe Trp Ala Tyr Lys Ile Tyr Tyr Val Tyr Gly Phe
115          340          345          350
118 Met Met Leu Val Leu Val Ile Leu Cys Ile Val Thr Val Cys Val Thr
119          355          360          365
122 Ile Val Cys Thr Tyr Phe Leu Leu Asn Ala Glu Asp Tyr Arg Trp Gln
123      370          375          380
126 Trp Thr Ser Phe Leu Ser Ala Ala Ser Thr Ala Ile Tyr Val Tyr Met
127 385          390          395          400
130 Tyr Ser Phe Tyr Tyr Tyr Phe Phe Lys Thr Lys Met Tyr Gly Leu Phe
131          405          410          415
134 Gln Thr Ser Phe Tyr Phe Gly Tyr Met Ala Val Phe Ser Thr Ala Leu
135          420          425          430
138 Gly Ile Met Cys Gly Ala Ile
139          435
142 <210> SEQ ID NO: 2
143 <211> LENGTH: 1317
144 <212> TYPE: DNA
145 <213> ORGANISM: Homo sapiens
147 <400> SEQUENCE: 2
148 atgtacatag atgatttacc aatatggggt attgttggtg aggctgatga aaatggagaa      60
150 gattactatc tttggacctt taaaaaactt gaaatagggt ttaatggaaa tcgaattggt      120
152 gatgttaatc taactagtga aggaaagggt aaactgggtc caaatactaa aatccagatg      180
154 tcatattcag taaaatggaa aaagtcagat gtgaaatttg aagatcgatt tgacaaatat      240
156 ottgatccgt ctttttttca acatcggatt cattggtttt caattttcaa ctcttcatg      300
158 atggtgatct tcttggtggg cttagtttca atgattttta tgagaacatt aagaaaagat      360
160 tatgctcggg acagtaaaga ggaagaaatg gatgatatgg atagagacct aggagatgaa      420
162 tatggatgga aacaggtgca tggagatgta tttagaccat caagtcaccc actgatattt      480
164 tctctctctg ttggttctgg atgtcagata tttgctgtgt ctctcatcgt tattattggt      540
166 gcaatgatag aagatttata tactgagagg ggatcaatgc tcagtacagc catatttgtc      600
168 tatgctgcta cgtctccagt gaatggttat tttggaggaa gtctgtatgc tagacaagga      660
170 ggaaggagat ggataaagca gatgtttatt ggggcattcc ttatcccagc tatggtgtgt      720
172 ggcactgcct tcttcatcaa tttcatagcc atttattacc atgcttcaag agccattcct      780

```

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174 tttggaacaa tgggtggccgt ttgtttgcatc tgtttttttg ttattcttcc tctaaatctt      840
176 gttggtacaa tacttgccg aaatctgtca ggtcagccca actttccttg tcgtgtcaat      900
178 gctgtgcctc gtcctatacc ggagaaaaaa tggttcatgg agcctgcggg tattgtttgc      960
180 ctgggtggaa ttttaccttt tggttcaatc tttattgaaa tgtatttcat cttcacgtct    1020
182 ttctgggcac ataagatcta ttatgtctat ggcttcatga tgctgggtgct ggttatcctg    1080
184 tgcattgtga ctgtctgtgt gactattgtg tgcacatatt ttctactaaa tgcagaagat    1140
186 taccggtggc aatggacaag ttttctctct gctgcatcaa ctgcaatcta tgtttacatg    1200
188 tattcctttt actactattt tttcaaaaca aagatgtatg gcttatttca aacatcattt    1260
190 tactttggat atatggcggg atttagcaca gccttgggga taatgtgtgg agcgatt      1317

```

193 &lt;210&gt; SEQ ID NO: 3

194 &lt;211&gt; LENGTH: 965

195 &lt;212&gt; TYPE: DNA

196 &lt;213&gt; ORGANISM: Homo sapiens

198 &lt;400&gt; SEQUENCE: 3

```

199 cagatgtcat attcagtaaa atggaaaaag tcagatgtga aatttgaaga tcgatttgac      60
201 aaatatcttg atccgtcctt ttttcaacat cggattcatt ggttttcaat tttcaactcc    120
203 ttcatgatgg tgatcttctt ggtgggctta gtttcaatga ttttaagtga aacattaaga    180
205 aaagattatg ctcggtacag taaagaggaa gaaatggatg atatggatag agacctagga    240
207 gatgaatatg gatggaaaca ggtgcatgga gatgtattta gaccatcaag tcacccactg    300
209 atatttttct ctctgattgg ttctggatgt cagatatttg ctgtgtctct catcggtatt    360
211 attgttgcaa tgatagaaga tttatatact gagaggggat caatgctcag tacagccata    420
213 tttgtctatg ctgctacgtc tccagtgaat ggttatttta gaggaagtct gtatgctaga    480
215 caaggaggaa ggagatggat aaagcagatg tttattgggg cattccttat cccagctatg    540
217 gtgtgtggca ctgccttctt catcaatttc atagccattt attaccatgc ttcaagagcc    600
219 attccttttg gaacaatggt ggccgtttgt tgcactctgt tttttgttat tcttctctta    660
221 aatcttgttg gtacaatact tggccgaaat ctgtcagggt agcccaactt tccttgctcg    720
223 gtcaatgctg tgcctcgtcc tataccggag aaaaaatggt tcatggagcc tgcggttatt    780
225 gtttgccctg gtggaatttt accttttggg tcaatcttta ttgaaatgta tttcatcttc    840
227 acgtctttct gggcatataa gatctattat gtctatggct tcatgatgct ggtgctgggt    900
229 atcctgtgca ttgtgactgt ctgtgtgact attgtgtgca catattttct actaaatgca    960
231 gaaga

```

234 &lt;210&gt; SEQ ID NO: 4

235 &lt;211&gt; LENGTH: 285

236 &lt;212&gt; TYPE: DNA

237 &lt;213&gt; ORGANISM: Homo sapiens

239 &lt;400&gt; SEQUENCE: 4

```

240 tcagtaaaat ggaaaaagtc agatgtgaaa tttgaagatc gatttgacaa atatcttgat      60
242 cgtctctttt ttcaacatcg gattcattgg ttttcaattt tcaactcctt catgatgggt    120
244 atcttcttgg tgggcttagt ttcaatgatt ttaatgagaa cattaagaaa agattatgct    180
246 cggtagagta aagaggaaga aatggatgat atggatagag acctaggaga tgaatatgga    240
248 tggaaacagg tgcattggaga tgtatttaga ccatcaagtc accca

```

251 &lt;210&gt; SEQ ID NO: 5

252 &lt;211&gt; LENGTH: 17

253 &lt;212&gt; TYPE: PRT

254 &lt;213&gt; ORGANISM: Artificial sequence

256 &lt;220&gt; FEATURE:

257 &lt;223&gt; OTHER INFORMATION: Peptide sequence

259 &lt;400&gt; SEQUENCE: 5

261 Asp Pro Ser Phe Phe Gln His Arg Ile His Trp Phe Ser Ile Phe Asn

*insufficient explanation - give**source  
of genetic  
material**(see item 11 on  
Enr summary sheet)*

## RAW SEQUENCE LISTING

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Input Set : A:\aoyama5001.ST25.txt

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```

262 1                5                10                15
265 Ser
269 <210> SEQ ID NO: 6
270 <211> LENGTH: 17
271 <212> TYPE: PRT
272 <213> ORGANISM: Artificial sequence
274 <220> FEATURE:
275 <223> OTHER INFORMATION: Peptide sequence
277 <220> FEATURE:
278 <221> NAME/KEY: MISC_FEATURE
279 <222> LOCATION: (3)..(3)
280 <223> OTHER INFORMATION: Xaa can by any amino acid
283 <400> SEQUENCE: 6
285 Asp Pro Xaa Phe Phe Gln His Arg Ile His Val Phe Ser Ile Phe Asn
286 1                5                10                15
289 His
293 <210> SEQ ID NO: 7
294 <211> LENGTH: 20
295 <212> TYPE: DNA
296 <213> ORGANISM: Artificial sequence
298 <220> FEATURE:
299 <223> OTHER INFORMATION: probe/primer
301 <400> SEQUENCE: 7
302 tcagtaaaat ggaaaaagtc
305 <210> SEQ ID NO: 8
306 <211> LENGTH: 20
307 <212> TYPE: DNA
308 <213> ORGANISM: Artificial sequence
310 <220> FEATURE:
311 <223> OTHER INFORMATION: probe/primer
313 <400> SEQUENCE: 8
314 tgggtgactt gatggtctaa
317 <210> SEQ ID NO: 9
318 <211> LENGTH: 19
319 <212> TYPE: DNA
320 <213> ORGANISM: Artificial sequence
322 <220> FEATURE:
323 <223> OTHER INFORMATION: probe/primer
325 <400> SEQUENCE: 9
326 gctgtgtctc tcatcgtaa
329 <210> SEQ ID NO: 10
330 <211> LENGTH: 20
331 <212> TYPE: DNA
332 <213> ORGANISM: Artificial sequence
334 <220> FEATURE:
335 <223> OTHER INFORMATION: probe/primer
337 <400> SEQUENCE: 10
338 ccatccatat tcatctccta
341 <210> SEQ ID NO: 11

```

## RAW SEQUENCE LISTING

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Input Set : A:\aoyama5001.ST25.txt

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```

342 <211> LENGTH: 21
343 <212> TYPE: DNA
344 <213> ORGANISM: Artificial sequence
346 <220> FEATURE:
347 <223> OTHER INFORMATION: probe/primer
349 <400> SEQUENCE: 11
350 cggtatagga cgaggcacag c
353 <210> SEQ ID NO: 12
354 <211> LENGTH: 18
355 <212> TYPE: DNA
356 <213> ORGANISM: Artificial sequence
358 <220> FEATURE:
359 <223> OTHER INFORMATION: probe/primer
361 <400> SEQUENCE: 12
362 actgaatatg acatctgg
365 <210> SEQ ID NO: 13
366 <211> LENGTH: 1800
367 <212> TYPE: DNA
368 <213> ORGANISM: Homo sapiens
370 <220> FEATURE:
371 <221> NAME/KEY: CDS
372 <222> LOCATION: (3)..(1730)
373 <223> OTHER INFORMATION:
375 <400> SEQUENCE: 13
376 cc gcc gcg ctg tgg ctg ctg ctg ctg ctg ccc cgg acc cgg gcg
377 Ala Ala Leu Trp Leu Leu Leu Leu Leu Leu Pro Arg Thr Arg Ala
378 1 5 10 15
380 gac gag cac gaa cac acg tat caa gat aaa gag gaa gtt gtc tta tgg
381 Asp Glu His Glu His Thr Tyr Gln Asp Lys Glu Glu Val Val Leu Trp
382 20 25 30
384 atg aat act gtt ggg ccc tac cat aat cgt caa gaa aca tat aag tac
385 Met Asn Thr Val Gly Pro Tyr His Asn Arg Gln Glu Thr Tyr Lys Tyr
386 35 40 45
388 ttt tca ctt cca ttc tgt gtg ggg tca aaa aaa agt atc agt cat tac
389 Phe Ser Leu Pro Phe Cys Val Gly Ser Lys Lys Ser Ile Ser His Tyr
390 50 55 60
392 cat gaa act ctg gga gaa gca ctt caa ggg gtt gaa ttg gaa ttt agt
393 His Glu Thr Leu Gly Glu Ala Leu Gln Gly Val Glu Leu Glu Phe Ser
394 65 70 75
396 ggt ctg gat att aaa ttt aaa gat gat gtg atg cca gcc act tac tgt
397 Gly Leu Asp Ile Lys Phe Lys Asp Asp Val Met Pro Ala Thr Tyr Cys
398 80 85 90 95
400 gaa att gat tta gat aaa gaa aag aga gat gca ttt gta tat gcc ata
401 Glu Ile Asp Leu Asp Lys Glu Lys Arg Asp Ala Phe Val Tyr Ala Ile
402 100 105 110
404 aaa aat cat tac tgg tac cag atg tac ata gat gat tta cca ata tgg
405 Lys Asn His Tyr Trp Tyr Gln Met Tyr Ile Asp Asp Leu Pro Ile Trp
406 115 120 125
408 ggt att gtt ggt gag gct gat gaa aat gga gaa gat tac tat ctt tgg

```

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/09/319,724

DATE: 09/12/2002  
TIME: 15:45:22

Input Set : A:\aoyama5001.ST25.txt  
Output Set: N:\CRF4\09122002\I319724.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:6; Xaa Pos. 3

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/09/319,724

DATE: 09/12/2002

TIME: 15:45:22

Input Set : A:\aoyama5001.ST25.txt

Output Set: N:\CRF4\09122002\I319724.raw

L:285 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0